



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/728,696

DATE: 08/27/2004

TIME: 11:50:30

Input Set : N:\Crf3\RULE60\10728696.raw  
 Output Set: N:\CRF4\08272004\J728696.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Williams, James A.  
 6 Thalley, Bruce S.

8 (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium  
 9 Botulinum Neurotoxin

11 (iii) NUMBER OF SEQUENCES: 82

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Medlen & Carroll  
 15 (B) STREET: 220 Montgomery Street, Suite 2200  
 16 (C) CITY: San Francisco  
 17 (D) STATE: California  
 18 (E) COUNTRY: United States of America  
 19 (F) ZIP: 94104

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk  
 23 (B) COMPUTER: IBM PC compatible  
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/10/728,696  
 29 (B) FILING DATE: 05-Dec-2003  
 30 (C) CLASSIFICATION: 424

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/704,159  
 33 (B) FILING DATE: 28-AUG-1996

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Ingolia, Diane E.  
 36 (B) REGISTRATION NUMBER: 40,027  
 37 (C) REFERENCE/DOCKET NUMBER: OPHD-02304

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 705-8410  
 41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 24 base pairs  
 48 (B) TYPE: nucleic acid  
 49 (C) STRANDEDNESS: single  
 50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 GGAAATTAG CTGCAGCATC TGAC

60 (2) INFORMATION FOR SEQ ID NO: 2:

ENTERED

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62 (i) SEQUENCE CHARACTERISTICS:  
 63 (A) LENGTH: 24 base pairs  
 64 (B) TYPE: nucleic acid  
 65 (C) STRANDEDNESS: single  
 66 (D) TOPOLOGY: linear  
 68 (ii) MOLECULE TYPE: DNA (genomic)  
 72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 74 TCTAGCAAAT TCGCTTGTGT TGAA 24  
 76 (2) INFORMATION FOR SEQ ID NO: 3:  
 78 (i) SEQUENCE CHARACTERISTICS:  
 79 (A) LENGTH: 20 base pairs  
 80 (B) TYPE: nucleic acid  
 81 (C) STRANDEDNESS: single  
 82 (D) TOPOLOGY: linear  
 84 (ii) MOLECULE TYPE: DNA (genomic)  
 88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 90 CTCGCATATA GCATTAGACC 20  
 92 (2) INFORMATION FOR SEQ ID NO: 4:  
 94 (i) SEQUENCE CHARACTERISTICS:  
 95 (A) LENGTH: 19 base pairs  
 96 (B) TYPE: nucleic acid  
 97 (C) STRANDEDNESS: single  
 98 (D) TOPOLOGY: linear  
 100 (ii) MOLECULE TYPE: DNA (genomic)  
 104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 106 CTATCTAGGC CTAAAGTAT 19  
 108 (2) INFORMATION FOR SEQ ID NO: 5:  
 110 (i) SEQUENCE CHARACTERISTICS:  
 111 (A) LENGTH: 8133 base pairs  
 112 (B) TYPE: nucleic acid  
 113 (C) STRANDEDNESS: single  
 114 (D) TOPOLOGY: linear  
 116 (ii) MOLECULE TYPE: DNA (genomic)  
 119 (ix) FEATURE:  
 120 (A) NAME/KEY: CDS  
 121 (B) LOCATION: 1..8130  
 124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 126 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT 48  
 127 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile  
 128 1 5 10 15  
 130 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA 96  
 131 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu  
 132 20 25 30  
 134 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA 144  
 135 Tyr Asn Lys Leu Thr Thr Asn Asn Glu Asn Lys Tyr Leu Gln Leu  
 136 35 40 45  
 138 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT 192  
 139 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr  
 140 50 55 60

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142	TCA	AGC	AGA	AAT	AGA	GCA	CTC	TCT	AAT	CTA	AAA	AAA	GAT	ATA	TTA	AAA	240
143	Ser	Ser	Arg	Asn	Arg	Ala	Leu	Ser	Asn	Leu	Lys	Lys	Asp	Ile	Leu	Lys	
144	65					70				75						80	
146	GAA	GTA	ATT	CTT	ATT	AAA	AAT	TCC	AAT	ACA	AGC	CCT	GTA	GAA	AAA	AAT	288
147	Glu	Val	Ile	Leu	Ile	Lys	Asn	Ser	Asn	Thr	Ser	Pro	Val	Glu	Lys	Asn	
148						85				90						95	
150	TTA	CAT	TTT	GTA	TGG	ATA	GGT	GGA	GAA	GTC	AGT	GAT	ATT	GCT	CTT	GAA	336
151	Leu	His	Phe	Val	Trp	Ile	Gly	Gly	Glu	Val	Ser	Asp	Ile	Ala	Leu	Glu	
152						100				105						110	
154	TAC	ATA	AAA	CAA	TGG	GCT	GAT	ATT	AAT	GCA	GAA	TAT	AAT	ATT	AAA	CTG	384
155	Tyr	Ile	Lys	Gln	Trp	Ala	Asp	Ile	Asn	Ala	Glu	Tyr	Asn	Ile	Lys	Leu	
156						115				120						125	
158	TGG	TAT	GAT	AGT	GAA	GCA	TTC	TTA	GTA	AAT	ACA	CTA	AAA	AAG	GCT	ATA	432
159	Trp	Tyr	Asp	Ser	Glu	Ala	Phe	Leu	Val	Asn	Thr	Leu	Lys	Lys	Ala	Ile	
160						130				135						140	
162	GTT	GAA	TCT	TCT	ACC	ACT	GAA	GCA	TTA	CAG	CTA	CTA	GAG	GAA	GAG	ATT	480
163	Val	Glu	Ser	Ser	Thr	Thr	Glu	Ala	Leu	Gln	Leu	Leu	Glu	Glu	Glu	Ile	
164	145					150				155						160	
166	CAA	AAT	CCT	CAA	TTT	GAT	AAT	ATG	AAA	TTT	TAC	AAA	AAA	AGG	ATG	GAA	528
167	Gln	Asn	Pro	Gln	Phe	Asp	Asn	Met	Lys	Phe	Tyr	Lys	Lys	Arg	Met	Glu	
168						165				170						175	
170	TTT	ATA	TAT	GAT	AGA	CAA	AAA	AGG	TTT	ATA	AAT	TAT	TAT	AAA	TCT	CAA	576
171	Phe	Ile	Tyr	Asp	Arg	Gln	Lys	Arg	Phe	Ile	Asn	Tyr	Tyr	Lys	Ser	Gln	
172						180				185						190	
174	ATC	AAT	AAA	CCT	ACA	GTA	CCT	ACA	ATA	GAT	GAT	ATT	ATA	AAG	TCT	CAT	624
175	Ile	Asn	Lys	Pro	Thr	Val	Pro	Thr	Ile	Asp	Asp	Ile	Ile	Lys	Ser	His	
176						195				200						205	
178	CTA	GTA	TCT	GAA	TAT	AAT	AGA	GAT	GAA	ACT	GTA	TTA	GAA	TCA	TAT	AGA	672
179	Leu	Val	Ser	Glu	Tyr	Asn	Arg	Asp	Glu	Thr	Val	Leu	Glu	Ser	Tyr	Arg	
180						210				215						220	
182	ACA	AAT	TCT	TTG	AGA	AAA	ATA	AAT	AGT	AAT	CAT	GGG	ATA	GAT	ATC	AGG	720
183	Thr	Asn	Ser	Leu	Arg	Lys	Ile	Asn	Ser	Asn	His	Gly	Ile	Asp	Ile	Arg	
184	225					230				235						240	
186	GCT	AAT	AGT	TTG	TTT	ACA	GAA	CAA	GAG	TTA	TTA	AAT	ATT	TAT	AGT	CAG	768
187	Ala	Asn	Ser	Leu	Phe	Thr	Glu	Gln	Glu	Leu	Leu	Asn	Ile	Tyr	Ser	Gln	
188						245				250						255	
190	GAG	TTG	TTA	AAT	CGT	GGA	AAT	TTA	GCT	GCA	GCA	TCT	GAC	ATA	GTA	AGA	816
191	Glu	Leu	Leu	Asn	Arg	Gly	Asn	Leu	Ala	Ala	Ala	Ser	Asp	Ile	Val	Arg	
192						260				265						270	
194	TTA	TTA	GCC	CTA	AAA	AAT	TTT	GGC	GGA	GTA	TAT	TTA	GAT	GTT	GAT	ATG	864
195	Leu	Leu	Ala	Leu	Lys	Asn	Phe	Gly	Gly	Val	Tyr	Leu	Asp	Val	Asp	Met	
196						275				280						285	
198	CTT	CCA	GGT	ATT	CAC	TCT	GAT	TTA	TTT	AAA	ACA	ATA	TCT	AGA	CCT	AGC	912
199	Leu	Pro	Gly	Ile	His	Ser	Asp	Leu	Phe	Lys	Thr	Ile	Ser	Arg	Pro	Ser	
200						290				295						300	
202	TCT	ATT	GGA	CTA	GAC	CGT	TGG	GAA	ATG	ATA	AAA	TTA	GAG	GCT	ATT	ATG	960
203	Ser	Ile	Gly	Leu	Asp	Arg	Trp	Glu	Met	Ile	Lys	Leu	Glu	Ala	Ile	Met	
204	305					310				315						320	
206	AAG	TAT	AAA	AAA	TAT	ATA	AAT	AAT	TAT	ACA	TCA	GAA	AAC	TTT	GAT	AAA	1008

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207	Lys	Tyr	Lys	Lys	Tyr	Ile	Asn	Asn	Tyr	Thr	Ser	Glu	Asn	Phe	Asp	Lys	
208							325				330					335	
210	CTT	GAT	CAA	CAA	TTA	AAA	GAT	AAT	TTT	AAA	CTC	ATT	ATA	GAA	AGT	AAA	1056
211	Leu	Asp	Gln	Gln	Leu	Lys	Asp	Asn	Phe	Lys	Leu	Ile	Glu	Ser	Lys		
212											340		345		350		
214	AGT	GAA	AAA	TCT	GAG	ATA	TTT	TCT	AAA	TTA	GAA	AAT	TTA	AAT	GTA	TCT	1104
215	Ser	Glu	Ser	Glu	Ile	Phe	Ser	Lys	Leu	Glu	Asn	Leu	Asn	Val	Ser		
216											355		360		365		
218	GAT	CTT	GAA	ATT	AAA	ATA	GCT	TTC	GCT	TTA	GGC	AGT	GTT	ATA	AAT	CAA	1152
219	Asp	Leu	Glu	Ile	Lys	Ile	Ala	Phe	Ala	Leu	Gly	Ser	Val	Ile	Asn	Gln	
220											370		375		380		
222	GCC	TTG	ATA	TCA	AAA	CAA	GGT	TCA	TAT	CTT	ACT	AAC	CTA	GTA	ATA	GAA	1200
223	Ala	Leu	Ile	Ser	Lys	Gln	Gly	Ser	Tyr	Leu	Thr	Asn	Leu	Val	Ile	Glu	
224											385		390		395		400
226	CAA	GTA	AAA	AAT	AGA	TAT	CAA	TTT	TTA	AAC	CAA	CAC	CTT	AAC	CCA	GCC	1248
227	Gln	Val	Lys	Asn	Arg	Tyr	Gln	Phe	Leu	Asn	Gln	His	Leu	Asn	Pro	Ala	
228											405		410		415		
230	ATA	GAG	TCT	GAT	AAT	AAC	TTC	ACA	GAT	ACT	ACT	AAA	ATT	TTT	CAT	GAT	1296
231	Ile	Glu	Ser	Asp	Asn	Asn	Phe	Thr	Asp	Thr	Thr	Lys	Ile	Phe	His	Asp	
232											420		425		430		
234	TCA	TTA	TTT	AAT	TCA	GCT	ACC	GCA	GAA	AAC	TCT	ATG	TTT	TTA	ACA	AAA	1344
235	Ser	Leu	Phe	Asn	Ser	Ala	Thr	Ala	Glu	Asn	Ser	Met	Phe	Leu	Thr	Lys	
236											435		440		445		
238	ATA	GCA	CCA	TAC	TTA	CAA	GTA	GGT	TTT	ATG	CCA	GAA	GCT	CGC	TCC	ACA	1392
239	Ile	Ala	Pro	Tyr	Leu	Gln	Val	Gly	Phe	Met	Pro	Glu	Ala	Arg	Ser	Thr	
240											450		455		460		
242	ATA	AGT	TTA	AGT	GGT	CCA	GGA	GCT	TAT	GCG	TCA	GCT	TAC	TAT	GAT	TTC	1440
243	Ile	Ser	Leu	Ser	Gly	Pro	Gly	Ala	Tyr	Ala	Ser	Ala	Tyr	Tyr	Asp	Phe	
244											465		470		475		480
246	ATA	AAT	TTA	CAA	GAA	AAT	ACT	ATA	GAA	AAA	ACT	TTA	AAA	GCA	TCA	GAT	1488
247	Ile	Asn	Leu	Gln	Glu	Asn	Thr	Ile	Glu	Lys	Thr	Leu	Lys	Ala	Ser	Asp	
248											485		490		495		
250	TTA	ATA	GAA	TTT	AAA	TTC	CCA	GAA	AAT	ATA	GCT	TCT	CAA	TTG	ACA	GAA	1536
251	Leu	Ile	Glu	Phe	Lys	Phe	Pro	Glu	Asn	Asn	Leu	Ser	Gln	Leu	Thr	Glu	
252											500		505		510		
254	CAA	GAA	ATA	AAT	AGT	CTA	TGG	AGC	TTT	GAT	CAA	GCA	AGT	GCA	AAA	TAT	1584
255	Gln	Glu	Ile	Asn	Ser	Leu	Trp	Ser	Phe	Asp	Gln	Ala	Ser	Ala	Lys	Tyr	
256											515		520		525		
258	CAA	TTT	GAG	AAA	TAT	GTA	AGA	GAT	TAT	ACT	GGT	GGA	TCT	CTT	TCT	GAA	1632
259	Gln	Phe	Glu	Lys	Tyr	Val	Arg	Asp	Tyr	Thr	Gly	Gly	Ser	Leu	Ser	Glu	
260											530		535		540		
262	GAC	AAT	GGG	GTA	GAC	TTT	AAT	AAA	AAT	ACT	GCC	CTC	GAC	AAA	AAC	TAT	1680
263	Asp	Asn	Gly	Val	Asp	Phe	Asn	Lys	Asn	Thr	Ala	Leu	Asp	Lys	Asn	Tyr	
264											545		550		555		560
266	TTA	TTA	AAT	AAT	AAA	ATT	CCA	TCA	AAC	AAT	GTA	GAA	GAA	GCT	GGA	AGT	1728
267	Leu	Leu	Asn	Asn	Lys	Ile	Pro	Ser	Asn	Asn	Val	Glu	Glu	Ala	Gly	Ser	
268											565		570		575		
270	AAA	AAT	TAT	GTT	CAT	TAT	ATC	ATA	CAG	TTA	CAA	GGA	GAT	GAT	ATA	AGT	1776
271	Lys	Asn	Tyr	Val	His	Tyr	Ile	Gln	Leu	Gln	Gly	Asp	Asp	Ile	Ser		

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272	580	585	590	
274	TAT GAA GCA ACA TGC AAT TTA TTT TCT AAA AAT CCT AAA AAT AGT ATT			1824
275	Tyr Glu Ala Thr Cys Asn Leu Phe Ser Lys Asn Pro Lys Asn Ser Ile			
276	595	600	605	
278	ATT ATA CAA CGA AAT ATG AAT GAA AGT GCA AAA AGC TAC TTT TTA AGT			1872
279	Ile Ile Gln Arg Asn Met Asn Glu Ser Ala Lys Ser Tyr Phe Leu Ser			
280	610	615	620	
282	GAT GAT GGA GAA TCT ATT TTA GAA TTA AAT AAA TAT AGG ATA CCT GAA			1920
283	Asp Asp Gly Glu Ser Ile Leu Glu Leu Asn Lys Tyr Arg Ile Pro Glu			
284	625	630	635	640
286	AGA TTA AAA AAT AAG GAA AAA GTA AAA GTA ACC TTT ATT GGA CAT GGT			1968
287	Arg Leu Lys Asn Lys Glu Lys Val Lys Val Thr Phe Ile Gly His Gly			
288	645	650	655	
290	AAA GAT GAA TTC AAC ACA AGC GAA TTT GCT AGA TTA AGT GTA GAT TCA			2016
291	Lys Asp Glu Phe Asn Thr Ser Glu Phe Ala Arg Leu Ser Val Asp Ser			
292	660	665	670	
294	CTT TCC AAT GAG ATA AGT TCA TTT TTA GAT ACC ATA AAA TTA GAT ATA			2064
295	Leu Ser Asn Glu Ile Ser Ser Phe Leu Asp Thr Ile Lys Leu Asp Ile			
296	675	680	685	
298	TCA CCT AAA AAT GTA GAA GTA AAC TTA CTT GGA TGT AAT ATG TTT AGT			2112
299	Ser Pro Lys Asn Val Glu Val Asn Leu Leu Gly Cys Asn Met Phe Ser			
300	690	695	700	
302	TAT GAT TTT AAT GTT GAA GAA ACT TAT CCT GGG AAG TTG CTA TTA AGT			2160
303	Tyr Asp Phe Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Ser			
304	705	710	715	720
306	ATT ATG GAC AAA ATT ACT TCC ACT TTA CCT GAT GTA AAT AAA AAT TCT			2208
307	Ile Met Asp Lys Ile Thr Ser Thr Leu Pro Asp Val Asn Lys Asn Ser			
308	725	730	735	
310	ATT ACT ATA GGA GCA AAT CAA TAT GAA GTA AGA ATT AAT AGT GAG GGA			2256
311	Ile Thr Ile Gly Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly			
312	740	745	750	
314	AGA AAA GAA CTT CTG GCT CAC TCA GGT AAA TGG ATA AAT AAA GAA GAA			2304
315	Arg Lys Glu Leu Leu Ala His Ser Gly Lys Trp Ile Asn Lys Glu Glu			
316	755	760	765	
318	GCT ATT ATG AGC GAT TTA TCT AGT AAA GAA TAC ATT TTT TTT GAT TCT			2352
319	Ala Ile Met Ser Asp Leu Ser Ser Lys Glu Tyr Ile Phe Phe Asp Ser			
320	770	775	780	
322	ATA GAT AAT AAG CTA AAA GCA AAG TCC AAG AAT ATT CCA GGA TTA GCA			2400
323	Ile Asp Asn Lys Leu Lys Ala Lys Ser Lys Asn Ile Pro Gly Leu Ala			
324	785	790	795	800
326	TCA ATA TCA GAA GAT ATA AAA ACA TTA TTA CTT GAT GCA AGT GTT AGT			2448
327	Ser Ile Ser Glu Asp Ile Lys Thr Leu Leu Asp Ala Ser Val Ser			
328	805	810	815	
330	CCT GAT ACA AAA TTT ATT TTA AAT AAT CTT AAG CTT AAT ATT GAA TCT			2496
331	Pro Asp Thr Lys Phe Ile Leu Asn Asn Leu Lys Leu Asn Ile Glu Ser			
332	820	825	830	
334	TCT ATT GGG GAT TAC ATT TAT TAT GAA AAA TTA GAG CCT GTT AAA AAT			2544
335	Ser Ile Gly Asp Tyr Ile Tyr Tyr Glu Lys Leu Glu Pro Val Lys Asn			
336	835	840	845	

**VERIFICATION SUMMARY**

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:4168 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32

L:11352 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=82